CLAIMS

We claim:

1. A method for generating a protozyme, said method comprising:

a) identifying a suitable protein scaffold lacking a desirable enzyme-like activity;

b) inputting a protein backbone structure of said protein scaffold into a computer, wherein said backbone structure has variable residue positions ;

c) inserting an active site domain into said scaffold;

d) applying at least one protein design cycle; and

e) generating a set of candidate variant proteins with putative enzyme-like activity.

2. A method according to claim 1 wherein said insertion step is done at the same time as said protein design cycle.

3. A method according to claim 1 wherein said insertion step is done prior to said applying step.

4. A method according to claim 1 wherein said insertion step is done after said applying step.

5. A method according to claim 1 wherein said insertion step comprises the use of at least one high energy state rotamer.

6. A method according to claim 1 further comprising applying a second protein design cycle prior to said generating step.

7. A method according to claim 1 wherein said active site domain catalyzes a known enzymatic reaction.

8. A method according to claim 1 wherein said active site domain catalyzes an unknown enzymatic reaction.

9. A method according to claim 1 wherein said active site domain is a ligand binding domain.

10. A method according to claim 1 wherein said protein design cycle comprises a DEE computation

11. A method according to claim 1 wherein said protein design cycle includes the use of at least one scoring function.

12. A method according to claim 8 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

13. A method according to claim 1 further comprising synthesizing a plurality of secondary sequences to generate a library of putative protoenzymes.

14. A method according to claim 13 wherein said synthesis includes a shuffling step.

15. A method according to claim 1 further comprising testing said candidate variant proteins for said catalytic property.

16. A method according to claim 1 wherein said protein design cycle comprises protein design automation.

17. A method according to claim 1 wherein said protein design cycle comprises a force field calculation.